

p2500usq.ST25.txt
SEQUENCE LISTING

<110> Medical Research Council
Choo, Yen
Klug, Aaron
Isalan, Mark

<120> Nucleic Acid Binding Polypeptide Library

<130> 71278/264974

<140> US 09/424,482

<141> 1999-11-23

<150> GB9710809.6

<151> 1997-05-23

<150> PCT/GB98/01510

<151> 1998-05-25

<160> 19

<170> PatentIn version 3.0

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<223> Description of Artificial Sequence: LIB-A DNA sorting
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<400> 1

gnnncggcg

9

<210> 2

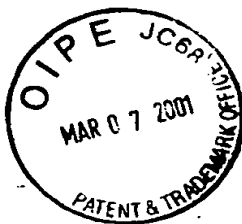
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31
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Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

<210> 5
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<223> Description of Artificial Sequence: Structure B

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<222> (3)..(6)

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<221> SITE

<222> (8)..(10)

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<222> (21)..(23)

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<221> VARIANT

<222> (8)..(10)

<223> 0-1 residue may be missing

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Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Leu Xaa Xaa His Xaa Xaa Xaa His
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<210> 6

<211> 4

<212> PRT

<213> Artificial

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<223> Description of Artificial Sequence: Linker

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Thr Gly Glu Lys
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<210> 7

<211> 5

<212> PRT

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<223> Description of Artificial Sequence: Linker

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Thr Gly Glu Lys Pro
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<210> 8

<211> 26

<212> PRT

<213> Artificial

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<223> Description of Artificial Sequence: Consensus structure

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Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Lys Ser Asp
1 5 10 15

Leu Val Lys His Gln Arg Thr His Thr Gly
20 25

<210> 9

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<211> 29
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 <223> Description of Artificial Sequence: Consensus structure
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Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro
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<210> 10
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Met Ala Glu Glu Lys Pro
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<223> Description of Artificial Sequence: Zinc finger -DNA
interaction sequence

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9

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<212> DNA

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<223> Description of Artificial Sequence: Zinc finger-DNA
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acgcccacg

9

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<212> DNA

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<223> Description of Artificial Sequence: Zinc finger-DNA
interaction sequence

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gcgtgggcg

9

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<223> Description of Artificial Sequence: Zinc finger-DNA
interaction library designed sequence

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finger

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Met Ala Glu Glu Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
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Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr
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Gly Gln Lys Pro
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B1

<210> 17
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Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asp Leu
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Thr Xaa His Ile Arg Thr His Thr Gly Glu Lys Pro
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<210> 18
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<212> PRT
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Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Xaa Ser Xaa Asp Arg
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Lys Arg His Thr Lys Ile His Leu Arg Gln Lys Asp
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<210> 19
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1 5 10 15
Lys Arg His Thr Lys Ile His Leu Arg Gln Lys Asp
20 25